



SEQUENCE LISTING

<110> Arkowitz, Robert A
Nern, Peter MA

<120> NUCLEOTIDE SEQUENCES AND PROTEIN
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<130> DYOU13.1A2CP1

<140> 10/054399

<141> 2002-01-21

<150> 09/168,474

<151> 1998-10-08

<150> 08/951,141

<151> 1997-10-15

<150> 09/529,106

<151> 2000-04-07

<150> US 09/732,180

<151> 2000-12-07

<150> US 60/169,699

<151> 1999-12-07

<150> PCT/GB98/03033

<151> 1998-10-08

<160> 37

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<213> *Saccharomyces cerevisiae*

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tttgcattta acgatgagga gcttttcaact atatccgacg tttttgccaa ctcgacgtcc 180
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<210> 2

<211> 76

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro

1

5

10

15

Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp

20

25

30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 3
<211> 228
<212> DNA
<213> Artificial Sequence

<220>
<223> cdc24-m1

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gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaaacac 120
tttgcattta acgatgagga gcttttcaact atatccgacg ttttgccaa ctcgacgtcc 180
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<210> 4
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> cdc24-m1

<400> 4
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15
Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 5
<211> 228
<212> DNA
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<220>
<223> cdc24-m2

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ggcgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaaacac 120
tttgcattta acgatgagga gcttttcaact atatccgacg ttttgccaa ctcgacgtcc 180
cagctggtca aagtgcgtaga agtagtagaa acgctaatga attccagc 228

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<210> 6
<211> 76
<212> PRT
<213> Artificial Sequence
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| <220>
<223> cdc24-m2

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<400> 6
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   1           5           10          15
Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
   20          25          30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
   35          40          45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
   50          55          60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
   65          70          75

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tttgcattta acgatgagga gcttttcaact atatccgacg tttttgccaa ctcgacgtcc 180
cagctggtca aagtgctaga agtagtagaa acgctaattga attccacgc 228
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<210> 8
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<212> PRT
<213> Artificial Sequence

<220>
<223> cdc24-m3

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<400> 8
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  20          25          30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
  35          40          45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
  50          55          60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
  65          70          75

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<210> 9

<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> Yeast cdc24p DH PH

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Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
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Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
35 40 45
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
50 55 60
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
65 70 75 80
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
85 90 95
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
100 105 110
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
115 120 125
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
130 135 140
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
145 150 155 160
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
165 170 175
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
180 185 190
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe
195 200 205
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Glu Pro Glu Arg
210 215 220
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Leu Phe Ser Glu
225 230 235 240
Val Val Thr Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Ser
245 250 255
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
260 265 270
Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser
275 280 285
Asn Asn Ile His Leu Ser Ser Ser Ala Ala Ala Ile Ile His Ser
290 295 300
Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser
305 310 315 320
Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
325 330 335
Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
340 345 350
Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
355 360 365
Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
370 375 380
Gln Leu Ile His Asp Leu Lys Asn

<210> 10
 <211> 1269
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 10
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 ccacaaagtc tacaggatat ctctgcagt gaggaagaaa ttcaaaataa aatagaggcc 120
 gccagacaag agagtaaaca gcttcatgt caaataaata aagcaaaaca caagatacaa 180
 gatgcaagct tattccagat gccaacaaa gttacttcgt tgacccaaaa taagatcaac 240
 ttaaagccaa atatcggtt gaaaggccat aataataaaa tctcagatt tcggtgagt 300
 cgagattcaa aacgtatTTT gagtgcaagt caagatggct ttatgctt atggacagt 360
 gcttcaggtt taaaacagaa cgcttattcca ttagattctc aatgggttct ttcctgcgt 420
 atttcgcccattt cgagtacttt ggttagcaagc gcaggattaa acaataactg taccatttat 480
 agagtttgcga aagaaaacag agtagcgc当地 aacgttgcgt caatTTTCAA aggacataact 540
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<210> 11
 <211> 422
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 11
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 Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
 20 25 30
 Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
 35 40 45
 His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
 50 55 60
 Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
 65 70 75 80
 Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
 85 90 95
 Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
 100 105 110
 Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
 115 120 125
 Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
 130 135 140
 Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr

145	150	155	160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe			
165	170	175	
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala			
180	185	190	
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile			
195	200	205	
Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val			
210	215	220	
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn			
225	230	235	240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser			
245	250	255	
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile			
260	265	270	
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser			
275	280	285	
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile			
290	295	300	
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro			
305	310	315	320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln			
325	330	335	
Thr Leu Lys Ser Thr Ser Ser Tyr Leu Asp Asn Gln Gly Val Val			
340	345	350	
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr			
355	360	365	
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly			
370	375	380	
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro			
385	390	395	400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile			
405	410	415	
Trp Ser Pro Gly Tyr Gln			
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<210> 12
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<213> Artificial Sequence

<220>
<223> ste4-o15

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gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaaca caagatacaa 180
gatgcaagct tattccagat gccaacaaa gttacttcgt tgacccaaaaa taagatcaac 240
ttaaagccaa atatcggtt gaaaggccat aataataaa tctcagatt tcggtgagt 300
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atTCGccat cgagtacttt ggttagcaagc gcaggattaa acaataactg taccattat 480
agatTTcga aagaaaacag agtagcgcaa aacgttgcgt caatTTcaa aggacatact 540
tgcttatTTT ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
atgacatgtg ctttgcggaa tataccgaaa gcaaaagaggg tgagaggata ttctgaccat 660

ttaggtgatg ttttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720
acattcgcta gctgtggatc agacgggtat acttacatat gggatagcag atctccgtcc 780
gctgtacaaa gctttacgt taacgatagt gatattaatg cacttcgttt tttcaaagac 840
gggatgtcga ttgtgcagg aagtgacaat ggtgcgataa atatgtatga tttaaggtcg 900
gactgttcta ttgctactt ttctttttt cgaggttatg aagaacgtac ccctaccct 960
acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
acaagctcaa gctatctaga caaccaaggc gttgttctt tagattttag tgcacatcgga 1080
agattgtatgt actcatgcta tacagacatt ggttgtgtt gttggatgt attaaaagga 1140
gagattgttggaaaattaga aggtcatggt ggcagagtca ctgggtgtcg ctcgagtcca 1200
gatgggttag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
tatcaatag 1269

<210> 13
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<212> PRT
<213> Artificial Sequence

<220>
<223> ste4-o15

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20 25 30
Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45
His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60
Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80
Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95
Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110
Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125
Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140
Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145 150 155 160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
195 200 205
Pro Lys Ala Lys Arg Val Arg Gly Tyr Ser Asp His Leu Gly Asp Val
210 215 220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225 230 235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
245 250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
260 265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
275 280 285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
 290 295 300
 Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
 305 310 315 320
 Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
 325 330 335
 Thr Leu Lys Ser Thr Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
 340 345 350
 Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
 355 360 365
 Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
 370 375 380
 Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
 385 390 395 400
 Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
 405 410 415
 Trp Ser Pro Gly Tyr Gln
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<210> 14
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 <212> DNA
 <213> Artificial Sequence

<220>
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 gccagacaag agagtaaaca gcttcatgt caaataaaata aagcaaaaca caagatacaa 180
 gatgcaagct tattccagat gccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
 ttaaagccaa atatcggtt gaaaggccat aataataaaa tctcagattt tcggtgagtt 300
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 gtttcaggTTT taaaacagaa cgcttattcA ttagattctc aatgggttct ttcctgcgt 420
 atttcgcat cgagtacttt gtagcaagc gcaggattaa acaataactg taccatttat 480
 agagtttcga aagaaaacag agtagcgcaa aacggtgcgt caatTTTcaa aggacatact 540
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 atgacatgtg ccttgggaa tataccgaaa gcaaagaggg tgagagaata ttctgaccat 660
 ttaggtgatg tttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720
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 gactgttcta ttgctacttt ttctctttt cgaggttatg aagaacgtac ccctaccct 960
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 acaagctcaa gctatctaga caaccaaggc gctgtttctt tagattttag tgcacatcgga 1080
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 gatgggttag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
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<210> 15
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>

<223> ste4-o17

<400> 15

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20 25 30
Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45
His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60
Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80
Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95
Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110
Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125
Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140
Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Cys Thr Ile Tyr
145 150 155 160
Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175
Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190
His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
195 200 205
Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
210 215 220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225 230 235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
245 250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
260 265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
275 280 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
290 295 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305 310 315 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
325 330 335
Thr Leu Lys Ser Thr Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val
340 345 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
355 360 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
370 375 380
Lys Leu Glu Gly His Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385 390 395 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
405 410 415
Trp Ser Pro Gly Tyr Gln

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope sequence

<400> 16
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease recognition sequence

<400> 17
Gln Asn Leu Tyr Phe Gln Gly
1 5

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> S. cerevisiae Cdc24-m1

<400> 18
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys
1 5 10 15
Lys Ser Ile

<210> 19
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> S. cerevisiae Cdc24-m2

<400> 19
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys
1 5 10 15
Lys Ser Ile

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> S. cervisiae Cdc24-m3

<400> 20
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys
1 5 10 15
Lys Ser Ile

<210> 21
<211> 19
<212> PRT
<213> Saccharomyces cerevisiae

<400> 21
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys
1 5 10 15
Lys Ser Ile

<210> 22
<211> 19
<212> PRT
<213> Homo sapien

<400> 22
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
1 5 10 15
Lys Thr Ile

<210> 23
<211> 2535
<212> DNA
<213> Candida albicans

<400> 23
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ttcaataaaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180
aaactacaaa aaatccctgg catggAACCA ttttgaacc aagcttcaa tcaggctgaa 240
caactcagtg aacaacaaggc attggctttg gcacaggaaa gaagcaatgg aaatggacat 300
agtaatggca aacgtcatca atcatttagac ggtgccatga atagacttgc agttggttct 360
gatagtagtt cgatccaagg ttcatcgaca cgaatggcca ccaatgcgtc aacgtcatct 420
ttaatcagtg gtatgccaaa caacaacact ttatttacgt ttactgcagg ggttttacca 480
gctaataatca gtgtcgatcc tgctacccat ctttggaaat tgttccaaca agggggcccc 540
ttttgtgttc ttatcaatca ttttttttttttccat taccagttgt cagttctgtat 600

gacttgagaa tttgcaaaaa atcagtatat gacttttaa ttgccgtcaa gacacaattg 660
 aattttgatg acgagaatat gttcaactata tccaatgttt tctccgacaa tgcccaagat 720
 ttaatcaaga ttattgatgt cattaataaa ctacttgctg agtactcaga tgctagtgac 780
 ctgggtggtg gcgatgaaga tgtaaatatg gatgttcaa ttaccatgaa aagatcaaaa 840
 gtttccgag aaattatcgaa aacagaaaaga aaatatgttc aagacttggaa actaatgtgt 900
 aaataccgtc aagatctaata tgaagccgaa aatttgtctt cagaacaaat tcacttggta 960
 ttcccaatt taaatgagat tattgatttt caaagacgat tcctcaatgg gttagaatgt 1020
 aacatcaatg tacctattag atatcaaaga attggatcag tatttattca tgcttcttg 1080
 gccccttca atgcttatgaa accttggact ataggacaat tgacggcgat tgatttgate 1140
 aacaaagaag ctgctaattt gaaaaaatcg tcaagtctac ttgatcctgg gttgaactt 1200
 caatcgatata tattaaagcc gatccaaaga ttgtgtaaat acccactttt gttgaaagag 1260
 ttaatcaaaa catcaccaga atattcaaaa caggaccccc atggcagctc gtcatcgaca 1320
 tcattcaatg aattattggt ggctaaaact gcaatgaaag aattggcaaa tcaagtcaat 1380
 gaggcgcaaa gacgagcaga aaatatcgaa cattggaaa aactaaaaga aagagtaggt 1440
 aattggcgtg ggttaattt ggatgctcaa ggagaactat tattccacgg acaagttggg 1500
 gttaaagatg ctgaaaatgaa aaaggaataac gttgcttatac ttttggaaa aatcgatattt 1560
 ttttcacag aaattgatgaa taccaaaaaa tctgatcaa acggaaaagaa gagcaagttt 1620
 tcgacaagaa agagatcaac ttcatcaat cttagttcat cgactactaa tttgttgaa 1680
 tcaataaaaca attccggaaa ggataaacaca ttgcattgg aattaaaggg aagagttat 1740
 atatcgaga ttataaacat ttccgcacca aacactcctg gctcaactct aatcatctca 1800
 tggtcaggta gaaaggaaag cggctcattt actttggat atcgtatgtgaaagccaga 1860
 aaccaatggg aaaagtgtt acgtgattt aagactaatg aaatgaataa acaaattcat 1920
 aagaagttac gtgattccga cctgtcattt aatactgatg actctgccccat atatgattac 1980
 acgggttata gtacgtcacc agtcaatcaa tcaactcaac aacaatacta tgatcatcg 2040
 ggctctcaca gttccgcacca tcactcatcg tcatccactt tgagtatgat gaagaataat 2100
 agagttaaat ctggtgattt gaggataata tcttcaactt caacaacatt agattcttc 2160
 agtaacaact tgaatgggtc accaaataacc actaatccat ctttgatgtc ttcagatgcc 2220
 accaaaacaa ttccaaacatt tgacgttgcatttaccaatgac gacagaattt 2280
 tcagagccat tgattgtcaa tgccacaattt gaggataatg accttttaca gaaaattatc 2340
 tcccagatta tcacttcgaa ctgggtggca gatgatgtca atattagtcg attgagat 2400
 aaagacgacg aaggagactt tggatattt aattcagatg atgattgggg gtttagtgctt 2460
 gatatgttaa ccagtgaaga cttttaccaa acatcaagca atgaaaaacg actggtgaca 2520
 gtgtgggtt cttga 2535

<210> 24

<211> 844

<212> PRT

<213> Candida albicans

<400> 24

Met	Glu	His	Pro	Pro	Ala	Ala	Leu	Arg	Thr	Phe	Ser	Thr	Gln	Ser	Thr
1									10				15		
Ser	Ser	Leu	Asn	Ser	Val	Ser	Thr	Val	Ser	Ser	Ser	Arg	Ile	Val	Ser
									20				25		30
Ser	Gly	Pro	Val	Asn	Ile	Asn	Asn	Phe	Asn	Lys	Pro	Ser	Thr	Pro	Lys
									35				40		45
Asp	His	Leu	Phe	Tyr	Arg	Cys	Glu	Ser	Leu	Lys	Arg	Lys	Leu	Gln	Lys
									50				55		60
Ile	Pro	Gly	Met	Glu	Pro	Phe	Leu	Asn	Gln	Ala	Phe	Asn	Gln	Ala	Glu
									65				70		75
Gln	Leu	Ser	Glu	Gln	Gln	Ala	Leu	Ala	Leu	Ala	Gln	Glu	Arg	Ser	Asn
									85				90		95
Gly	Asn	Gly	His	Ser	Asn	Gly	Lys	Arg	His	Gln	Ser	Leu	Asp	Gly	Ala
									100				105		110
Met	Asn	Arg	Leu	Ser	Val	Gly	Ser	Asp	Ser	Ser	Ser	Ile	Gln	Gly	Ser
									115				120		125
Leu	Thr	Arg	Met	Ala	Thr	Asn	Ala	Ser	Thr	Ser	Ser	Leu	Ile	Ser	Gly

130	135	140
Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val Leu Pro		
145	150	155
Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu Phe Gln		
165	170	175
Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser		
180	185	190
Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser		
195	200	205
Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp		
210	215	220
Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp		
225	230	235
Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr Ser		
245	250	255
Asp Ala Ser Asp Ser Gly Gly Asp Glu Asp Val Asn Met Asp Val		
260	265	270
Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile Glu Thr		
275	280	285
Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr Arg Gln		
290	295	300
Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His Leu Leu		
305	310	315
Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe Leu Asn		
325	330	335
Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg Ile Gly		
340	345	350
Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr Glu Pro		
355	360	365
Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys Glu Ala		
370	375	380
Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe Glu Leu		
385	390	395
Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr Pro Leu		
405	410	415
Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys Gln Asp		
420	425	430
Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu Val Ala		
435	440	445
Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala Gln Arg		
450	455	460
Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg Val Gly		
465	470	475
Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu Phe His		
485	490	495
Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr Val Ala		
500	505	510
Tyr Leu Phe Glu Lys Ile Val Phe Phe Thr Glu Ile Asp Asp Thr		
515	520	525
Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys		
530	535	540
Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu		
545	550	555
Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys		
565	570	575
Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr		
580	585	590

Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly
 595 600 605
 Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu
 610 615 620
 Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His
 625 630 635 640
 Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala
 645 650 655
 Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr
 660 665 670
 Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His
 675 680 685
 Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser
 690 695 700
 Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe
 705 710 715 720
 Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met
 725 730 735
 Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys
 740 745 750
 Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala
 755 760 765
 Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile
 770 775 780
 Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr
 785 790 795 800
 Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp
 805 810 815
 Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser
 820 825 830
 Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser
 835 840

<210> 25
 <211> 22
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 25
 Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser
 1 5 10 15
 Ile Tyr Asp Phe Ile Leu
 20

<210> 26
 <211> 22
 <212> PRT
 <213> *Candida albicans*

<400> 26
 Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
 1 5 10 15
 Val Tyr Asp Phe Leu Ile
 20

<210> 27

<211> 854

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 27

Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu
1 5 10 15
Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val
20 25 30
Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala
35 40 45
Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu
50 55 60
Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu
65 70 75 80
Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala
85 90 95
Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ile
100 105 110
Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn
115 120 125
Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe
130 135 140
Ser Met Gly Ile Leu Pro Ile Thr Met Asp Cys Asp Pro Val Thr Gln
145 150 155 160
Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu Cys Ile Leu Phe Asn
165 170 175
Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu
180 185 190
Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile Leu Gly Cys Lys Lys
195 200 205
His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr Ile Ser Asp Val Phe
210 215 220
Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu Glu Val Val Glu Thr
225 230 235 240
Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser Lys Ser Lys Thr Gln
245 250 255
Gln Ile Met Asn Ala Glu Asn Gln His Arg His Gln Pro Gln Gln Ser
260 265 270
Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile Lys Glu Phe Val Ala
275 280 285
Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile Leu Asp Lys Tyr Arg
290 295 300
Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser Glu Glu Leu Tyr Met
305 310 315 320
Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe Gln Arg Arg Phe Leu
325 330 335
Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro Ser Lys Gln Arg Ile
340 345 350
Gly Ala Leu Phe Met His Ser Lys His Phe Phe Lys Leu Tyr Glu Pro
355 360 365
Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe Leu Ser Ser Thr Leu
370 375 380
His Lys Met Arg Val Asp Glu Ser Gln Arg Phe Ile Ile Asn Asn Lys
385 390 395 400

Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val Gln Arg Leu Cys Arg
 405 410 415
 Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu Ser Ser Asp Asp Asn
 420 425 430
 Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile Ser Lys Asn Ile Ala
 435 440 445
 Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu Asn His Gln Val Val
 450 455 460
 Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser
 465 470 475 480
 Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr
 485 490 495
 Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu
 500 505 510
 Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser
 515 520 525
 Ser Leu Ile Leu Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala
 530 535 540
 Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys
 545 550 555 560
 Arg His Ser Asn Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser
 565 570 575
 Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn Ser Ser Asp Asn Asn
 580 585 590
 Ser Asn Asn Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu
 595 600 605
 Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln
 610 615 620
 Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile
 625 630 635 640
 Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg
 645 650 655
 Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn
 660 665 670
 Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser
 675 680 685
 Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr
 690 695 700
 Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe
 705 710 715 720
 Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg
 725 730 735
 Thr Thr Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn
 740 745 750
 Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr
 755 760 765
 Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu
 770 775 780
 Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser
 785 790 795 800
 Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser Pro Ile Thr Lys Ile
 805 810 815
 Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val Leu Gly Ser Asp Glu
 820 825 830
 Asp Trp Asn Val Ala Lys Glu Met Leu Ala Glu Asn Asn Glu Lys Phe
 835 840 845
 Leu Asn Ile Arg Leu Tyr

<210> 28
 <211> 837
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 28
 Ser Gly Thr Ser Leu Ser Asp Leu Lys Pro Lys Pro Ser Ala Thr Ser
 1 5 10 15
 Ile Ser Ile Pro Met Gln Asn Val Met Asn Lys Pro Val Thr Glu Gln
 20 25 30
 Asp Ser Leu Phe His Ile Cys Ala Asn Ile Arg Lys Arg Leu Glu Val
 35 40 45
 Leu Pro Gln Leu Lys Pro Phe Leu Gln Leu Ala Tyr Gln Ser Ser Glu
 50 55 60
 Val Leu Ser Glu Arg Gln Ser Leu Leu Leu Ser Gln Lys Gln His Gln
 65 70 75 80
 Glu Leu Leu Lys Ser Asn Gly Ala Asn Arg Asp Ser Ser Asp Leu Ala
 85 90 95
 Pro Thr Leu Arg Ser Ser Ser Ile Ser Thr Ala Thr Ser Leu Met Ser
 100 105 110
 Met Glu Gly Ile Ser Tyr Thr Asn Ser Asn Pro Ser Ala Thr Pro Asn
 115 120 125
 Met Glu Asp Thr Leu Leu Thr Phe Ser Met Gly Ile Leu Pro Ile Thr
 130 135 140
 Met Asp Cys Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gly
 145 150 155 160
 Ala Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu
 165 170 175
 Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr
 180 185 190
 Asp Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu
 195 200 205
 Leu Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val
 210 215 220
 Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile
 225 230 235 240
 Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln
 245 250 255
 His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val
 260 265 270
 Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp
 275 280 285
 Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
 290 295 300
 Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
 305 310 315 320
 Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
 325 330 335
 Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
 340 345 350
 His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
 355 360 365
 Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
 370 375 380

Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
 385 390 395 400
 Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
 405 410 415
 Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
 420 425 430
 Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
 435 440 445
 Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
 450 455 460
 Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe
 465 470 475 480
 Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Glu Pro Glu Arg
 485 490 495
 Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Leu Phe Ser Glu
 500 505 510
 Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Ser
 515 520 525
 Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
 530 535 540
 Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser
 545 550 555 560
 Asn Asn Ile His Leu Ser Ser Ser Ala Ala Ala Ile Ile His Ser
 565 570 575
 Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser
 580 585 590
 Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
 595 600 605
 Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
 610 615 620
 Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
 625 630 635 640
 Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
 645 650 655
 Gln Leu Ile His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His
 660 665 670
 Ser Ser Thr Ser Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met
 675 680 685
 Ser Pro Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln
 690 695 700
 Thr His Asp Ser Met Ala Ser Phe Ser Ser His Met Lys Arg Val
 705 710 715 720
 Ser Asp Val Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser
 725 730 735
 Glu Ile Lys Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser
 740 745 750
 Ser Ile Leu Phe Arg Ile Ser Tyr Asn Asn Ser Asn Asn Thr Ser
 755 760 765
 Ser Ser Glu Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp
 770 775 780
 Asp Leu Ile Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn
 785 790 795 800
 Asn Ile Ser Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp
 805 810 815
 Phe Val Val Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu Met
 820 825 830
 Leu Ala Glu Asn Asn

<210> 29
 <211> 813
 <212> PRT
 <213> Candida albicans

<400> 29
 Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile
 1 5 10 15
 Val Ser Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr
 20 25 30
 Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu
 35 40 45
 Gln Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln
 50 55 60
 Ala Glu Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg
 65 70 75 80
 Ser Asn Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp
 85 90 95
 Gly Ala Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln
 100 105 110
 Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile
 115 120 125
 Ser Gly Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val
 130 135 140
 Leu Pro Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu
 145 150 155 160
 Phe Gln Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro
 165 170 175
 Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
 180 185 190
 Lys Ser Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe
 195 200 205
 Asp Asp Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala
 210 215 220
 Gln Asp Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu
 225 230 235 240
 Tyr Ser Asp Ala Ser Asp Ser Gly Gly Asp Glu Asp Val Asn Met
 245 250 255
 Asp Val Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile
 260 265 270
 Glu Thr Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr
 275 280 285
 Arg Gln Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His
 290 295 300
 Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe
 305 310 315 320
 Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg
 325 330 335
 Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr
 340 345 350
 Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys
 355 360 365
 Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe
 370 375 380

Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr
 385 390 395 400
 Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys
 405 410 415
 Gln Asp Pro His Gly Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu
 420 425 430
 Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala
 435 440 445
 Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg
 450 455 460
 Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu
 465 470 475 480
 Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr
 485 490 495
 Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Thr Glu Ile Asp
 500 505 510
 Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr
 515 520 525
 Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Thr Thr Asn Leu
 530 535 540
 Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu
 545 550 555 560
 Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro
 565 570 575
 Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu
 580 585 590
 Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln
 595 600 605
 Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
 610 615 620
 Ile His Lys Lys Leu Arg Asp Ser Asp Ser Phe Asn Thr Asp Asp
 625 630 635 640
 Ser Ala Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln
 645 650 655
 Ser Thr Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg
 660 665 670
 His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val
 675 680 685
 Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp
 690 695 700
 Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser
 705 710 715 720
 Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala
 725 730 735
 Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val
 740 745 750
 Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln
 755 760 765
 Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu
 770 775 780
 Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp
 785 790 795 800
 Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp
 805 810

<211> 684

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 30

Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
1 5 10 15
Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
20 25 30
Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
35 40 45
Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr
50 55 60
Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
65 70 75 80
Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
85 90 95
Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His
100 105 110
Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile
115 120 125
Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile
130 135 140
Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser
145 150 155 160
Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe
165 170 175
Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro
180 185 190
Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys His Phe Phe
195 200 205
Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe
210 215 220
Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser Gln Arg Phe
225 230 235 240
Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val
245 250 255
Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu
260 265 270
Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile
275 280 285
Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu
290 295 300
Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys
305 310 315 320
Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val
325 330 335
Phe Ile Ser Thr Thr Asn Ser Ser Glu Pro Glu Arg Glu Phe Glu
340 345 350
Val Tyr Leu Phe Glu Lys Ile Ile Leu Phe Ser Glu Val Val Thr
355 360 365
Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Ser Ser Thr Ser
370 375 380
Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His
385 390 395 400
His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Asn Asn Ile
405 410 415

His Leu Ser Ser Ser Ala Ala Ala Ile His Ser Ser Thr Asn
 420 425 430
 Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Leu Phe Lys
 435 440 445
 Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile
 450 455 460
 Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile
 465 470 475 480
 Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys
 485 490 495
 Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile
 500 505 510
 His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr
 515 520 525
 Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr
 530 535 540
 Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp
 545 550 555 560
 Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val
 565 570 575
 Leu Pro Lys Arg Arg Thr Thr Ser Ser Phe Glu Ser Glu Ile Lys
 580 585 590
 Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu
 595 600 605
 Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu
 610 615 620
 Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile
 625 630 635 640
 Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser
 645 650 655
 Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val
 660 665 670
 Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu
 675 680

<210> 31
 <211> 742
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 31

Asp	Pro	Val	Thr	Glu	Ile	Trp	Leu	Phe	Cys	Arg	Leu	Gly	Tyr	Pro	Leu	
1				5			10			15						
Cys	Ala	Leu	Phe	Asn	Cys	Leu	Pro	Val	Lys	Gln	Lys	Leu	Glu	Val	Asn	
				20			25			30						
Ser	Ser	Val	Ser	Leu	Glu	Asn	Thr	Asn	Val	Cys	Lys	Ala	Ser	Leu	Tyr	
				35			40			45						
Arg	Phe	Met	Leu	Met	Cys	Lys	Asn	Glu	Leu	Gly	Leu	Thr	Asp	Ala	Ala	
	50				55			60								
Leu	Phe	Ser	Ile	Ser	Glu	Ile	Tyr	Lys	Pro	Ser	Thr	Ala	Pro	Leu	Val	
	65				70			75			80					
Arg	Ala	Leu	Gln	Thr	Ile	Glu	Leu	Leu	Lys	Lys	Tyr	Glu	Val	Ser		
					85			90			95					
Asn	Thr	Thr	Lys	Ser	Ser	Ser	Thr	Pro	Ser	Pro	Ser	Thr	Asp	Asp	Asn	
				100			105			110						
Val	Pro	Thr	Gly	Thr	Leu	Asn	Ser	Leu	Ile	Ala	Ser	Gly	Arg	Arg	Val	

115	120	125
Thr Ala Glu Leu Tyr Glu	Thr Glu Leu Lys Tyr	Ile Gln Asp Leu Glu
130	135	140
Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln	Lys Gln Ile Leu Ser	
145	150	155
Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu	Ile Leu Asp	
165	170	175
Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu	Ser Leu Pro	
180	185	190
Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ala Leu Glu	Gly	
195	200	205
Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn	Ala Gln Gln	
210	215	220
Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala	Asn Leu Leu	
225	230	235
Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro	Ile Gln Arg	
245	250	255
Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys	Gly Thr Pro	
260	265	270
Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met	Ala Cys Val	
275	280	285
Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg	Ile His Glu Asn	
290	295	300
Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile	Asp Trp Lys Gly	
305	310	315
Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp	Val Val Asn	
325	330	335
Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val	Tyr Leu Phe Glu	
340	345	350
Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu	Lys Arg Gln Ala	
355	360	365
Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu	Asp Ser Leu Gln	
370	375	380
Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr	Val Val Pro Asn	
385	390	395
His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg	Gly Asp Pro	
405	410	415
Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu	Glu Ser His Lys	
420	425	430
Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys	Asn Glu His Gly	
435	440	445
Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro	Ala Asn Pro Val	
450	455	460
Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly	Tyr Asn Ser Ser Asp	
465	470	475
Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn	Val Asn Ser Pro	
485	490	495
Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro	Phe Thr Lys Thr	
500	505	510
Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Asp Glu	Arg Pro Ser	
515	520	525
Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val	Gly Thr Ser Ser Leu	
530	535	540
Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn	Asp Ser Ser Ser	
545	550	555
Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser	Gln Val Asn Ser	
565	570	575

Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val
 580 585 590
 Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr
 595 600 605
 Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp
 610 615 620
 Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys
 625 630 635 640
 Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser
 645 650 655
 Ser Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys
 660 665 670
 Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His
 675 680 685
 Asp Ile Thr Phe Asp Glu Leu Leu Ala Lys Val Glu His Lys Ile Lys
 690 695 700
 Leu Cys Gly Ile Leu Lys Gln Ala Val Pro Phe Arg Val Arg Leu Lys
 705 710 715 720
 Tyr Val Asp Glu Asp Gly Asp Phe Ile Thr Ile Thr Ser Asp Glu Asp
 725 730 735
 Val Leu Met Ala Phe Glu
 740

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <221> misc_feature
 <222> 12
 <223> n = A,T,C or G

 <221> misc_feature
 <222> 3, 7, 18
 <223> r = A or G

 <221> misc_feature
 <222> 6, 15
 <223> y = C or T

 <221> misc_feature
 <222> 9
 <223> k = G or T

 <221> misc_feature
 <222> 12
 <223> n = A,T,C or G

 <400> 32
 aartayrtkc angayttrga

<210> 33
 <211> 18

20

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
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<223> n = A,T,C or G

<221> misc_feature
<222> 1, 10, 15, 16
<223> r = A or G

<221> misc_feature
<222> 7
<223> y = C or T

<221> misc_feature
<222> 13
<223> n = A,T,C or G

<400> 33
ratttttytcr aanarrta

18

<210> 34
<211> 76
<212> PRT
<213> Candida albicans

<400> 34
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15
Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30
Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
35 40 45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60
Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr
65 70 75

<210> 35
<211> 19
<212> PRT
<213> Candida albicans

<400> 35
Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
1 5 10 15
Lys Ser Val

<210> 36
<211> 73

<212> PRT

<213> Candida albicans

<400> 36

Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15
Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30
Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
35 40 45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60
Ile Ile Asp Val Ile Asn Lys Leu Leu
65 70

<210> 37

<211> 73

<212> PRT

<213> Saccharomyces cerevisiae

<400> 37

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15
Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met
65 70